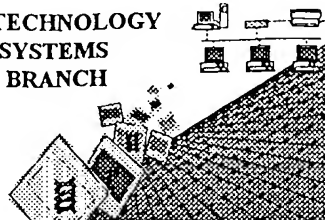


VW

BIOTECHNOLOGY
SYSTEMS
BRANCH



#6

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/009,030

Source:

P48/10

Date Processed by STIC:

11/6/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/009,030

TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

<input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
<input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
<input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
<input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
<input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
<input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
<input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
<input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
<input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
<input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
<input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
<input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
<input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCF/10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002
TIME: 14:11:23

Input Set : A:\410.txt
Output Set: N:\CRF4\11062002\J009030.raw

9 <110> APPLICANT: Arand, Michel
10 Archelas, Alain Robert
11 Baratti, Jacques
12 Furstoss, Roland
14 <120> TITLE OF INVENTION: PROTEINS WITH FUNGICIDAL ORIGIN AND DERIVATIVES, THEIR
15 PROCESS OF OBTENTION, AND THEIR USES, NAMELY FOR THE
16 PREPARATION OF ENANTIOMERICALLY PURE MOLECULES
18 <130> FILE REFERENCE: 410.018
20 <140> CURRENT APPLICATION NUMBER: 10/009,030
21 <141> CURRENT FILING DATE: 2000-11-02
23 <160> NUMBER OF SEQ ID NOS: 2
25 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1197
29 <212> TYPE: DNA
30 <213> ORGANISM: Aspergillus niger
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1197)

Does Not Comply
Corrected Diskette Needed

36 Nucleotide Sequence SEQ ID NO : 1

37 <400> SEQUENCE: 1
38 atg tcc gct ccg ttc gcc aag ttt ccc tcg tcg gcg agc att tcg cct 48
39 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
40 1 5 10 15
42 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96
--> 43 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu (Gln) Leu Asp Asp Leu Lys
--> 44 20 25 invalid 30 35 ← misaligned number
46 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
47 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
48 35 40 45
50 caa gcg gat ggc cgg ttt gcc atc act tct gaa tgg ctg aca act atg 192
51 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
52 50 55 60
54 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
55 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
56 65 70 75 80
58 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
59 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
60 85 90 95

delete this - it is not necessary

(see item 3
on Error
summary
sheet)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002

TIME: 14:11:23

Input Set : A:\410.txt

Output Set: N:\CRF4\11062002\J009030.raw

```

62   cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336
63   His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
--> 64       100              105              110
66   ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384
67   Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
--> 68       115              120              125
70   cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg 432
71   Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
--> 72       130              135              140
--> 74   gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg 480
75   Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
--> 76       145              150              155              160
78   gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg 528
79   Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
--> 80       165              170              175
82   atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat 576
83   Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
--> 84       180              185              190
86   att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc 624
87   Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
--> 88       195              200              205
90   aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc 672
91   Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
--> 92       210              215              220
94   ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga 720
95   Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
--> 96       225              230              235              240
98   atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt 768
99   Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
--> 100      245 align this number 250      255
102   act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca 816
103   Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
--> 104      260              265              270
106   tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc 864
107   Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
--> 108      275              280              285
110   ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg 912
111   Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
--> 112      290              295              300
117   gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act 960
118   Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
--> 119      305              310              315              320
121   gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008
122   Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
--> 123      325              330              335
125   cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg 1056
126   His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
--> 127      340              345              350
129   cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104

```

O/C

align nos. directly
under
amino acid

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002
TIME: 14:11:23

Input Set : A:\410.txt

Output Set: N:\CRF4\11062002\J009030.raw

```

130   Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
--> 131           355           360           365
133   cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152
134   His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
--> 135           370           375           380
137   aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197
--> 138   Lys Thr Asp Leu Thr Ala Phe Val Glu Gin Val Trp Gin Lys
--> 139           385           390           395
--> 141   Peptide sequence SEQ ID NO : 2
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 399
--> 144 <212> TYPE: mandatory response (insert PRT)
145 <213> ORGANISM: Aspergillus niger
147 <400> SEQUENCE: 2
148   Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
149       1           5           10           15
151   Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gin Leu Asp Asp Leu Lys
152           20           25           30
154   Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
155           35           40           45
157   Gin Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
158       50           55           60
160   Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
161       65           70           75           80
163   Leu Asn Ser Phe Pro Gin Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
164           85           90           95
166   His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
167           100          105          110
169   Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
170           115          120          125
173   Gin Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
174       130          135          140
176   Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
177       145          150          155          160
179   Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gin Leu
180           165          170          175
182   Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gin Gly Gly Asp
183           180          185          190
185   Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
186           195          200          205
188   Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
189           210          215          220
191   Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
192       225          230          235          240
194   Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
195           245          250          255
197   Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
198           260          265          270
200   Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro

```

398 shown below

invalid
amino acid
designator
(multiple
appearances
in the sequence)

move line over
so that
numbers
appear
directly
under
amino-
acids

RAW SEQUENCE LISTING

DATE: 11/06/2002

PATENT APPLICATION: US/10/009,030

TIME: 14:11:23

Input Set : A:\410.txt

Output Set: N:\CRF4\11062002\J009030.raw

```

201          275          280          285
203  Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
204          290          295          300
206  Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
207  305          310          315          320
209  Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
210          325          330          335
212  His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
213          340          345          350
215  Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
216          355          360          365
218  His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
219          370          375          380
221  Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
222  385          390          395

```

delete one
space

only one

space

between
amino acids

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,030

DATE: 11/06/2002

TIME: 14:11:24

Input Set : A:\410.txt

Output Set: N:\CRF4\11062002\J009030.raw

:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:37 M:283 W: Missing Blank Line separator, <400> field identifier
:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:74 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
:141 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1196
:141 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:1220 SEQ:1
:141 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
:141 M:112 C: (48) String data converted to lower case,
:141 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1197 Found:1220 SEQ:1
:144 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: